



SEQUENCE LISTING

<110> Skånemejerier AB

<120> NEW ENZYME AND ITS USE

<130> 75086

<150> US 60/320,139

<151> 2003-04-24

<150> US 60/481,598

<151> 2003-11-05

<160> 18

<170> PatentIn version 3.2

<210> 1

<211> 458

<212> PRT

<213> Unknown

<220>

<223> Unknown

<400> 1

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Ala Pro Gly Ala Gly Ala Pro Val Gln Ser Gln Gly Ser Gln Asn Lys
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Leu Leu Leu Val Ser Phe Asp Gly Phe Arg Trp Asn Tyr Asp Gln Asp
35 40 45

Val Asp Thr Pro Asn Leu Asp Ala Met Ala Arg Asp Gly Val Lys Ala
50 55 60

Arg Tyr Met Thr Pro Ala Phe Val Thr Met Thr Ser Pro Cys His Phe
65 70 75 80

Thr Leu Val Thr Gly Lys Tyr Ile Glu Asn His Gly Val Val His Asn
85 90 95

Met Tyr Tyr Asn Thr Thr Ser Lys Val Lys Leu Pro Tyr His Ala Thr
100 105 110

Leu Gly Ile Gln Arg Trp Trp Asp Asn Gly Ser Val Pro Ile Trp Ile
115 120 125

Thr Ala Gln Arg Gln Gly Leu Arg Ala Gly Ser Phe Phe Tyr Pro Gly

130		135		140
Gly Asn Val Thr Tyr Gln Gly Val Ala Val Thr Arg Ser Arg Lys Glu				
145		150	155	160
Gly Ile Ala His Asn Tyr Lys Asn Glu Thr Glu Trp Arg Ala Asn Ile				
	165		170	175
Asp Thr Val Met Ala Trp Phe Thr Glu Glu Asp Leu Asp Leu Val Thr				
	180		185	190
Leu Tyr Phe Gly Glu Pro Asp Ser Thr Gly His Arg Tyr Gly Pro Glu				
	195		200	205
Ser Pro Glu Arg Arg Glu Met Val Arg Gln Val Asp Arg Thr Val Gly				
	210		215	220
Tyr Leu Arg Glu Ser Ile Ala Arg Asn His Leu Thr Asp Arg Leu Asn				
225		230	235	240
Leu Ile Ile Thr Ser Asp His Gly Met Thr Thr Val Asp Lys Arg Ala				
	245		250	255
Gly Asp Leu Val Glu Phe His Lys Phe Pro Asn Phe Thr Phe Arg Asp				
	260		265	270
Ile Glu Phe Glu Leu Leu Asp Tyr Gly Pro Asn Gly Met Leu Leu Pro				
	275		280	285
Lys Glu Gly Arg Leu Glu Lys Val Tyr Asp Ala Leu Lys Asp Ala His				
	290		295	300
Pro Lys Leu His Val Tyr Lys Lys Glu Ala Phe Pro Glu Ala Phe His				
305		310	315	320
Tyr Ala Asn Asn Pro Arg Val Thr Pro Leu Leu Met Tyr Ser Asp Leu				
	325		330	335
Gly Tyr Val Ile His Gly Arg Ile Asn Val Gln Phe Asn Asn Gly Glu				
	340		345	350
His Gly Phe Asp Asn Lys Asp Met Asp Met Lys Thr Ile Phe Arg Ala				
	355		360	365
Val Gly Pro Ser Phe Arg Ala Gly Leu Glu Val Glu Pro Phe Glu Ser				
	370		375	380

Val His Val Tyr Glu Leu Met Cys Arg Leu Leu Gly Ile Val Pro Glu
 385 390 395 400

Ala Asn Asp Gly His Leu Ala Thr Leu Leu Pro Met Leu His Thr Glu
 405 410 415

Ser Ala Leu Pro Pro Asp Ala Leu Leu Val Ala Asp Gly Pro Cys Leu
 420 425 430

Pro Ser Leu Ser Gln Ala Lys Gly Cys Met Pro Leu Ser Pro Ala Ala
 435 440 445

Pro Thr Pro Ala Trp Leu Leu Trp Cys Trp
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<210> 2
 <211> 1701
 <212> DNA
 <213> Unknown

<220>
 <223> Unknown

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 120
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 180
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 240
 tgaccagccc ctgccacttc accctggtca ccggcaaata tatcgagaac cacggggtgg
 300
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 360
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 420
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 540
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660

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720

acctcacaga ccgcctcaac ctgatcatca catccgacca cggcatgacg accgtggaca
780

aacgggctgg cgacctggtt gaattccaca agttcccca cttcaccttc cgggacatcg
840

agtttgagct cctggactac ggaccaaacg ggatgctgct ccctaaagaa gggaggctgg
900

agaaggtgta cgatgccctc aaggacgccc accccaagct ccacgtctac aagaaggagg
960

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1020

gcgaccttg ctacgtcatc catgggagaa ttaacgtcca gttcaacaat ggggagcacg
1080

gctttgacaa caaggacatg gacatgaaga ccatcttccg cgctgtgggc cctagcttca
1140

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1200

tgctgggcat cgtgccccgag gccaacgatg ggcacctagc tactctgctg cccatgctgc
1260

acacagaatc tgctcttccg cctgatgctc tgctggtcgc ggacggacct tgcctccca
1320

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1380

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1440

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1500

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1560

ttctgcgggc gctggaacct gcagaccgg cctcggtcag ctgggagggg cccgccccgg
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1680

aaaaaaaaaa aaaaaaaaaa a
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<210> 3
<211> 18
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<213> Unknown

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<400> 3

Ala Phe Val Thr Met Thr Ser Pro Cys His Phe Thr Leu Val Thr Gly
1 5 10 15

Lys Tyr

<210> 4

<211> 458

<212> PRT

<213> Unknown

<220>

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<400> 4

Met Arg Gly Pro Ala Val Leu Leu Thr Val Ala Leu Ala Thr Leu Leu
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Ala Pro Gly Ala Gly Ala Pro Val Gln Ser Gln Gly Ser Gln Asn Lys
20 25 30

Leu Leu Leu Val Ser Phe Asp Gly Phe Arg Trp Asn Tyr Asp Gln Asp
35 40 45

Val Asp Thr Pro Asn Leu Asp Ala Met Ala Arg Asp Gly Val Lys Ala
50 55 60

Arg Tyr Met Thr Pro Ala Phe Val Thr Met Thr Ser Pro Cys His Phe
65 70 75 80

Thr Leu Val Thr Gly Lys Tyr Ile Glu Asn His Gly Val Val His Asn
85 90 95

Met Tyr Tyr Asn Thr Thr Ser Lys Val Lys Leu Pro Tyr His Ala Thr
100 105 110

Leu Gly Ile Gln Arg Trp Trp Asp Asn Gly Ser Val Pro Ile Trp Ile
115 120 125

Thr Ala Gln Arg Gln Gly Leu Arg Ala Gly Ser Phe Phe Tyr Pro Gly
130 135 140

Gly Asn Val Thr Tyr Gln Gly Val Ala Val Thr Arg Ser Arg Lys Glu
 145 150 155 160

Gly Ile Ala His Asn Tyr Lys Asn Glu Thr Glu Trp Arg Ala Asn Ile
 165 170 175

Asp Thr Val Met Ala Trp Phe Thr Glu Glu Asp Leu Asp Leu Val Thr
 180 185 190

Leu Tyr Phe Gly Glu Pro Asp Ser Thr Gly His Arg Tyr Gly Pro Glu
 195 200 205

Ser Pro Glu Arg Arg Glu Met Val Arg Gln Val Asp Arg Thr Val Gly
 210 215 220

Tyr Leu Arg Glu Ser Ile Ala Arg Asn His Leu Thr Asp Arg Leu Asn
 225 230 235 240

Leu Ile Ile Thr Ser Asp His Gly Met Thr Thr Val Asp Lys Arg Ala
 245 250 255

Gly Asp Leu Val Glu Phe His Lys Phe Pro Asn Phe Thr Phe Arg Asp
 260 265 270

Ile Glu Phe Glu Leu Leu Asp Tyr Gly Pro Asn Gly Met Leu Leu Pro
 275 280 285

Lys Glu Gly Arg Leu Glu Lys Val Tyr Asp Ala Leu Lys Asp Ala His
 290 295 300

Pro Lys Leu His Val Tyr Lys Lys Glu Ala Phe Pro Glu Ala Phe His
 305 310 315 320

Tyr Ala Asn Asn Pro Arg Val Thr Pro Leu Leu Met Tyr Ser Asp Leu
 325 330 335

Gly Tyr Val Ile His Gly Arg Ile Asn Val Gln Phe Asn Asn Gly Glu
 340 345 350

His Gly Phe Asp Asn Lys Asp Met Asp Met Lys Thr Ile Phe Arg Ala
 355 360 365

Val Gly Pro Ser Phe Arg Ala Gly Leu Glu Val Glu Pro Phe Glu Ser
 370 375 380

Val His Val Tyr Glu Leu Met Cys Arg Leu Leu Gly Ile Val Pro Glu

385

390

395

400

Ala Asn Asp Gly His Leu Ala Thr Leu Leu Pro Met Leu His Thr Glu
 405 410 415

Ser Ala Leu Pro Pro Asp Gly Arg Pro Thr Leu Leu Pro Lys Gly Arg
 420 425 430

Ser Ala Leu Pro Pro Ser Ser Arg Pro Leu Leu Val Met Gly Leu Leu
 435 440 445

Gly Thr Val Ile Leu Leu Ser Glu Val Ala
 450 455

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 <212> DNA
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 120

tcctggtgtc cttcgacggc ttccgctgga actacgacca ggacgtggac accccaacc
 180

tggacgccat ggcccagac ggggtgaagg cacgctacat gacccccgcc tttgtcacca
 240

tgaccagccc ctgccacttc accctgggtca ccggcaaata tatcgagaac cacgggggtgg
 300

ttcacaacat gtactacaac accaccagca aggtgaagct gccctaccac gccacgctgg
 360

gcatccagag gtggtgggac aacggcagcg tgcccatctg gatcacagcc cagaggcagg
 420

gcctgagggc tggctccttc ttctaccggg gcgggaacgt cacctaccaa ggggtggctg
 480

tgacgcggag ccggaaagaa ggcacgcac acaactacaa aaatgagacg gagtggagag
 540

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acttcgggga gccggactcc acgggccaca ggtacggccc cgagtccccg gagaggaggg
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agatggtgcg gcagggtggac cggaccgtgg gctacctccg ggagagcatc gcgcgcaacc
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acctcacaga ccgcctcaac ctgatcatca catccgacca cggcatgacg accgtggaca
 780

aacgggctgg cgacctggtt gaattccaca agttcccaa cttcaccttc cgggacatcg
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 900

agaangtgta cgatgccctc aaggacgccc accccaagct ccacgtctac aagaaggagg
 960

cgttccccga ggccttcac tacgccaaca accccagggt cacaccctg ctgatgtaca
 1020

gcgaccttg ctacgtcatc catgggagaa ttaacgtcca gttcaacaat ggggagcacg
 1080

gctttgacaa caaggacatg gacatgaaga ccatcttccg cgctgtgggc cctagcttca
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 1200

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 1260

acacagaatc tgctcttccg cctgatggaa ggcctactct cctgccccag ggaagatctg
 1320

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 1380

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 1500

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caaaacccgc tcccgaagcg gcgctgccgt ctgcagccac gcgggggccc gcgggagctc
 1740

tgccggcgct ggaacctgca gacccggcct cggtcagctg ggagggggccc gccccggcac
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aaaaaaaaaa aaaaaaaaaa
1878

<210> 6
<211> 415
<212> PRT
<213> Unknown

<220>
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<400> 6

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Ala Pro Gly Ala Gly Ala Pro Val Gln Ser Gln Gly Ser Gln Asn Lys
20 25 30

Leu Leu Leu Val Ser Phe Asp Gly Phe Arg Trp Asn Tyr Asp Gln Asp
35 40 45

Val Asp Thr Pro Asn Leu Asp Ala Met Ala Arg Asp Gly Val Lys Ala
50 55 60

Arg Tyr Met Thr Pro Ala Phe Val Thr Met Thr Ser Pro Cys His Phe
65 70 75 80

Thr Leu Val Thr Gly Lys Tyr Ile Glu Asn His Gly Val Val His Asn
85 90 95

Met Tyr Tyr Asn Thr Thr Ser Lys Val Lys Leu Pro Tyr His Ala Thr
100 105 110

Leu Gly Ile Gln Arg Trp Trp Asp Asn Gly Ser Val Pro Ile Trp Ile
115 120 125

Thr Ala Gln Arg Gln Gly Leu Arg Ala Gly Ser Phe Phe Tyr Pro Gly
130 135 140

Gly Asn Val Thr Tyr Gln Gly Val Ala Val Thr Arg Ser Arg Lys Glu
145 150 155 160

Gly Ile Ala His Asn Tyr Lys Asn Glu Thr Glu Trp Arg Ala Asn Ile

165	170	175
Asp Thr Val Met Ala Trp Phe Thr Glu Glu Asp Leu Asp Leu Val Thr 180 185 190		
Leu Tyr Phe Gly Glu Pro Asp Ser Thr Gly His Arg Tyr Gly Pro Glu 195 200 205		
Ser Pro Glu Arg Arg Glu Met Val Arg Gln Val Asp Arg Thr Val Gly 210 215 220		
Tyr Leu Arg Glu Ser Ile Ala Arg Asn His Leu Thr Asp Arg Leu Asn 225 230 235 240		
Leu Ile Ile Thr Ser Asp His Gly Met Thr Thr Val Asp Lys Arg Ala 245 250 255		
Gly Asp Leu Val Glu Phe His Lys Phe Pro Asn Phe Thr Phe Arg Asp 260 265 270		
Ile Glu Phe Glu Leu Leu Asp Tyr Gly Pro Asn Gly Met Leu Leu Pro 275 280 285		
Lys Glu Gly Arg Leu Glu Lys Val Tyr Asp Ala Leu Lys Asp Ala His 290 295 300		
Pro Lys Leu His Val Tyr Lys Lys Glu Ala Phe Pro Glu Ala Phe His 305 310 315 320		
Tyr Ala Asn Asn Pro Arg Val Thr Pro Leu Leu Met Tyr Ser Asp Leu 325 330 335		
Gly Tyr Val Ile His Gly Arg Ile Asn Val Gln Phe Asn Asn Gly Glu 340 345 350		
His Gly Phe Asp Asn Lys Asp Met Asp Met Lys Thr Ile Phe Arg Ala 355 360 365		
Val Gly Pro Ser Phe Arg Ala Gly Leu Glu Val Glu Pro Phe Glu Ser 370 375 380		
Val His Val Tyr Glu Leu Met Cys Arg Leu Leu Gly Ile Val Pro Glu 385 390 395 400		
Ala Asn Asp Gly His Leu Ala Thr Leu Leu Pro Met Leu His Thr 405 410 415		

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<212> PRT
<213> Unknown

<220>
<223> Unknown

<400> 7

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<212> PRT
<213> Unknown

<220>
<223> Unknown

<400> 8

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<211> 7
<212> PRT
<213> Unknown

<220>
<223> Unknown

<400> 9

Pro	Thr	Lys	Thr	Phe	Pro	Asn
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<212> DNA
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<220>
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<210> 11
<211> 27
<212> DNA
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<220>
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<210> 12
<211> 20
<212> DNA
<213> Unknown

<220>
<223> Unknown

<400> 12
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20

<210> 13
<211> 18
<212> DNA
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<220>
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<400> 13
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<210> 14
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<212> DNA
<213> Unknown

<220>
<223> Unknown

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<211> 23
<212> DNA
<213> Unknown

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<210> 16
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<212> PRT
<213> Unknown

<220>
<223> Unknown

<400> 16

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<212> DNA
<213> Unknown

<220>
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<210> 18
<211> 31
<212> DNA
<213> Unknown

<220>
<223> Unknown

<400> 18
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